

Figure 1B

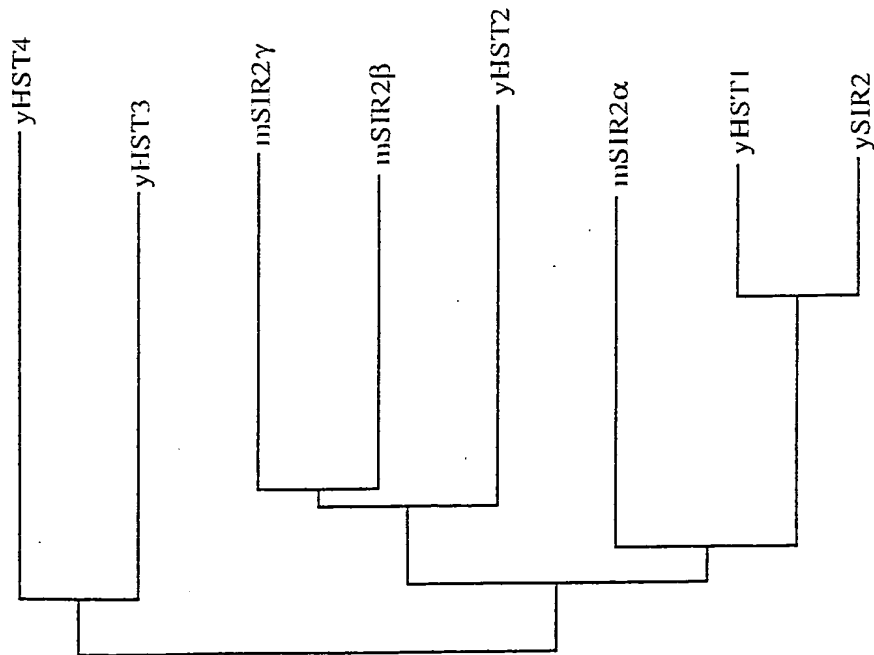


Figure 1A

ySIR2α 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

Figure 2C

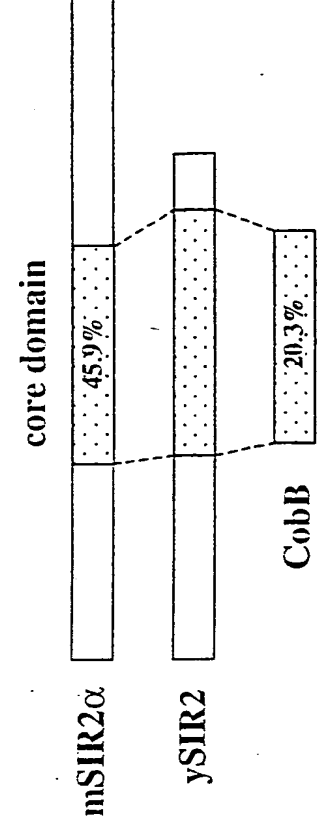


Figure 2D

Figure 2A

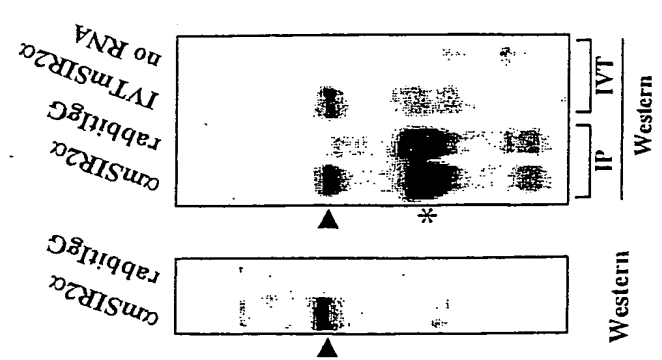


Figure 2B

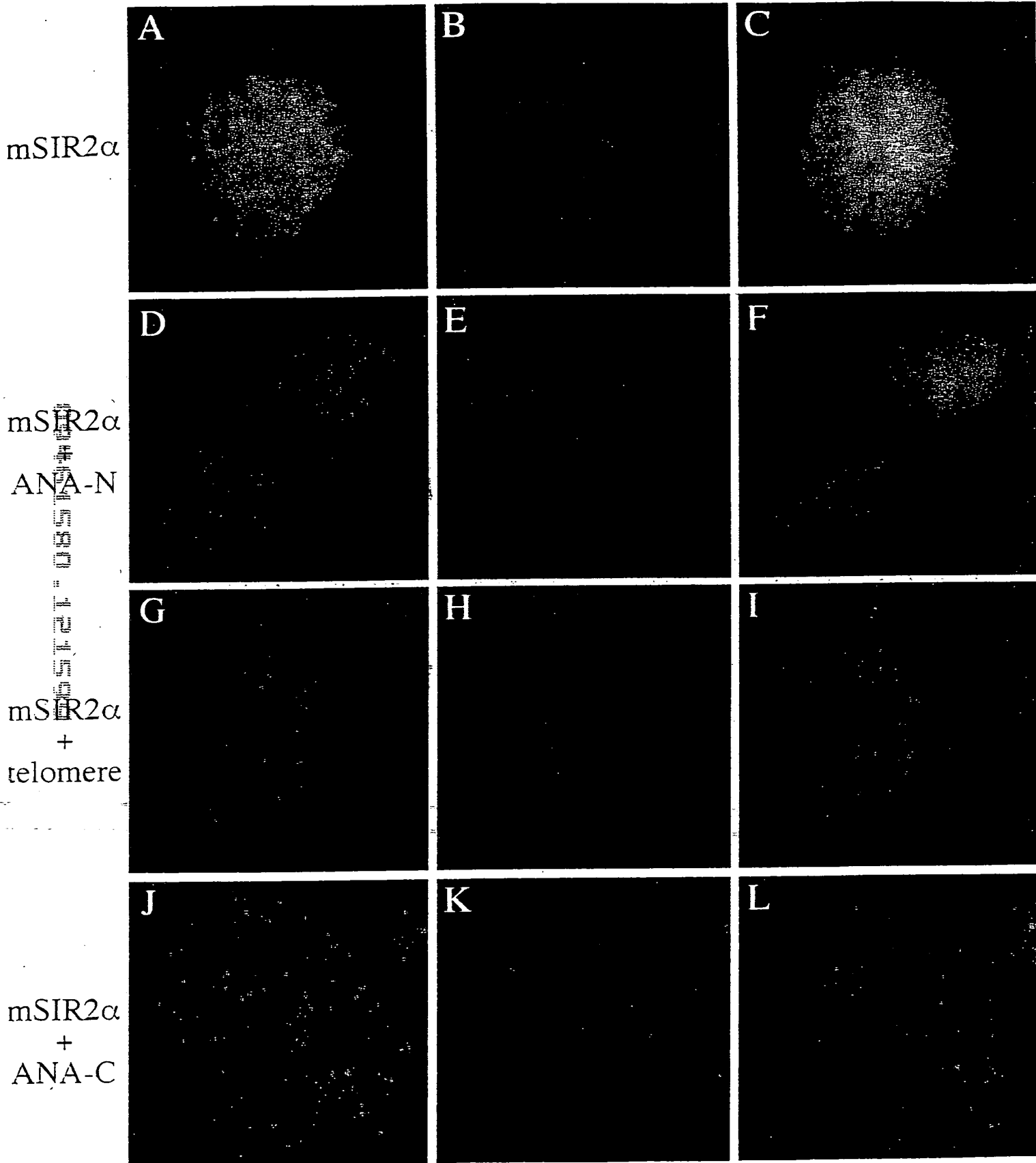


Figure 3

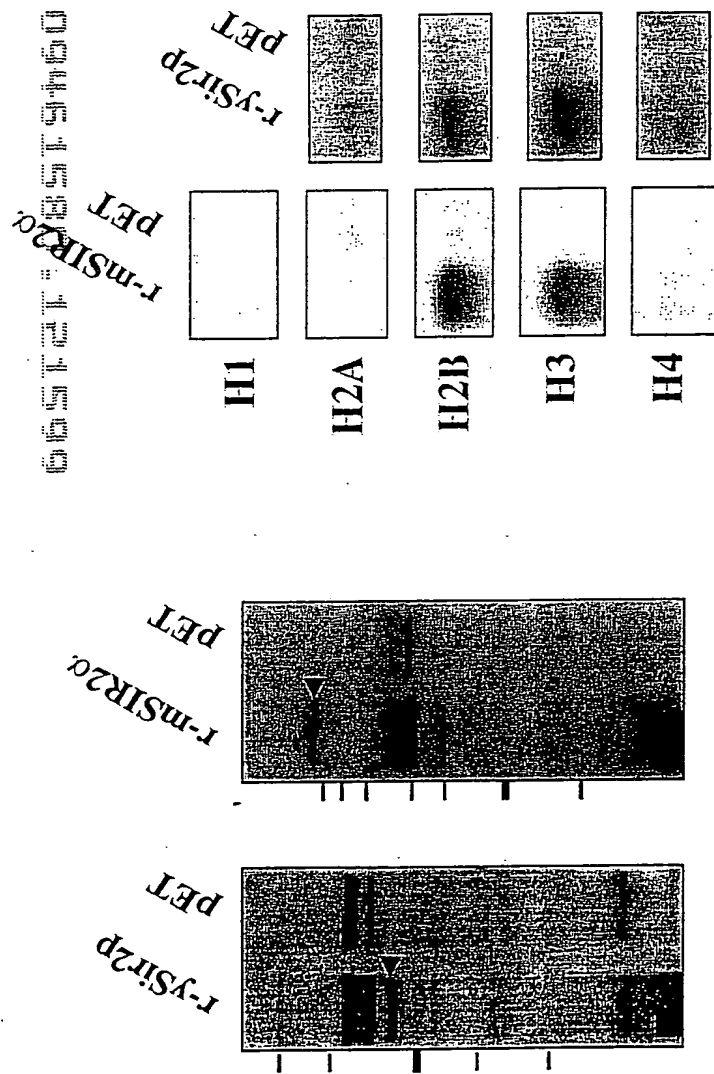


Figure 4A

Figure 4B

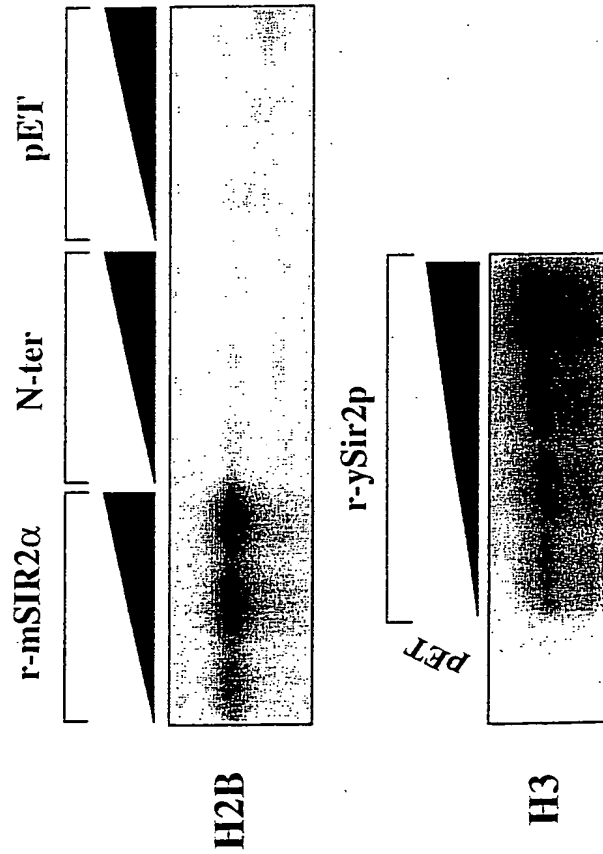


Figure 4D

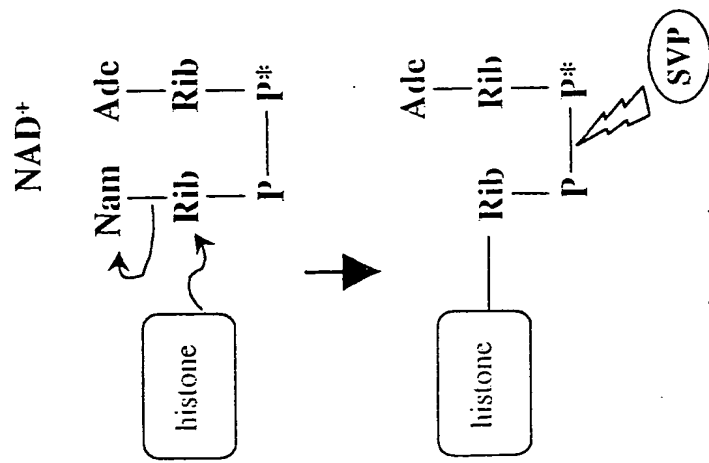


Figure 4C

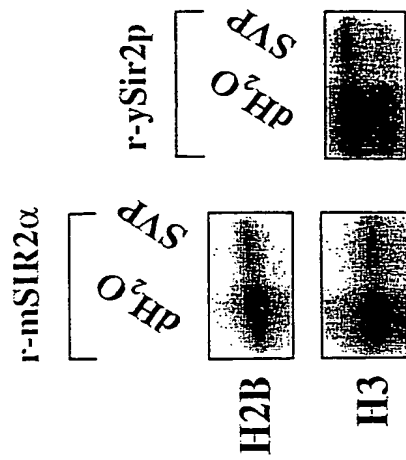


Figure 4E

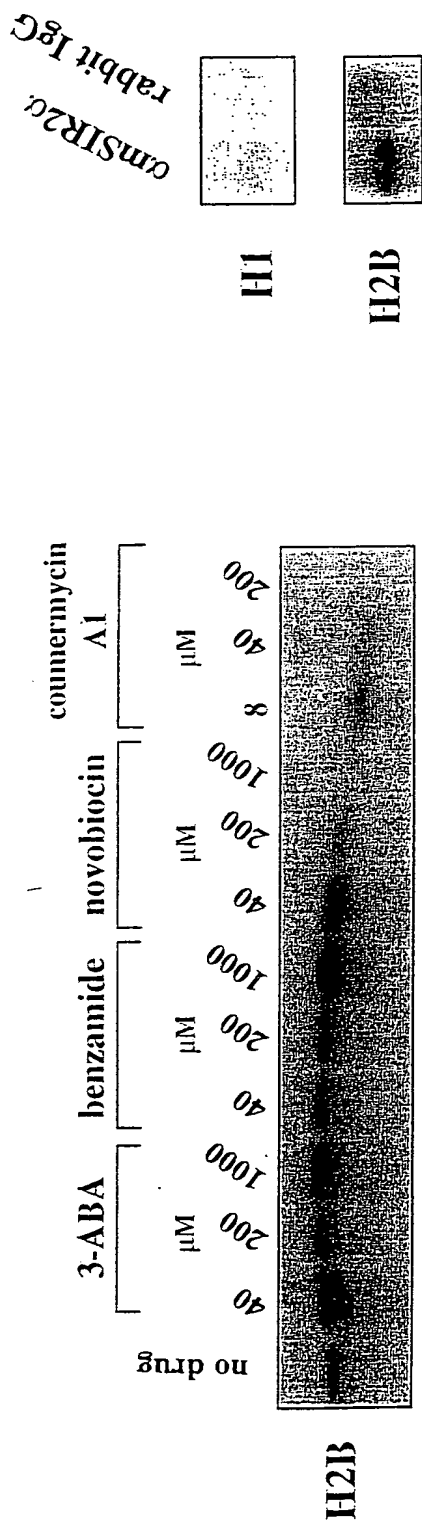


Figure 4G

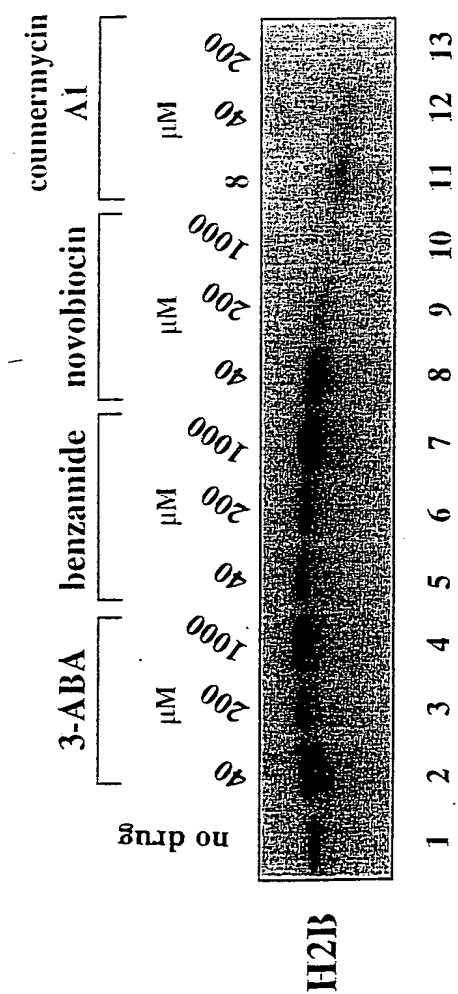


Figure 4F

### III

unAc                      \*                      \*  
diAc                      ARTKQTARKSTGGKAPRKQLC

H4

|         |                            |          |          |           |           |
|---------|----------------------------|----------|----------|-----------|-----------|
| monoAc  | <b>SGRGKGKGLKGGAKRHRC</b>  | <b>*</b> | <b>*</b> | <b>*</b>  | <b>*</b>  |
|         |                            | <b>5</b> | <b>8</b> | <b>12</b> | <b>16</b> |
| tetraAc | <b>AGGKGKGKMGKVGAKRHSC</b> | <b>*</b> | <b>*</b> | <b>*</b>  | <b>*</b>  |

Figure 5A

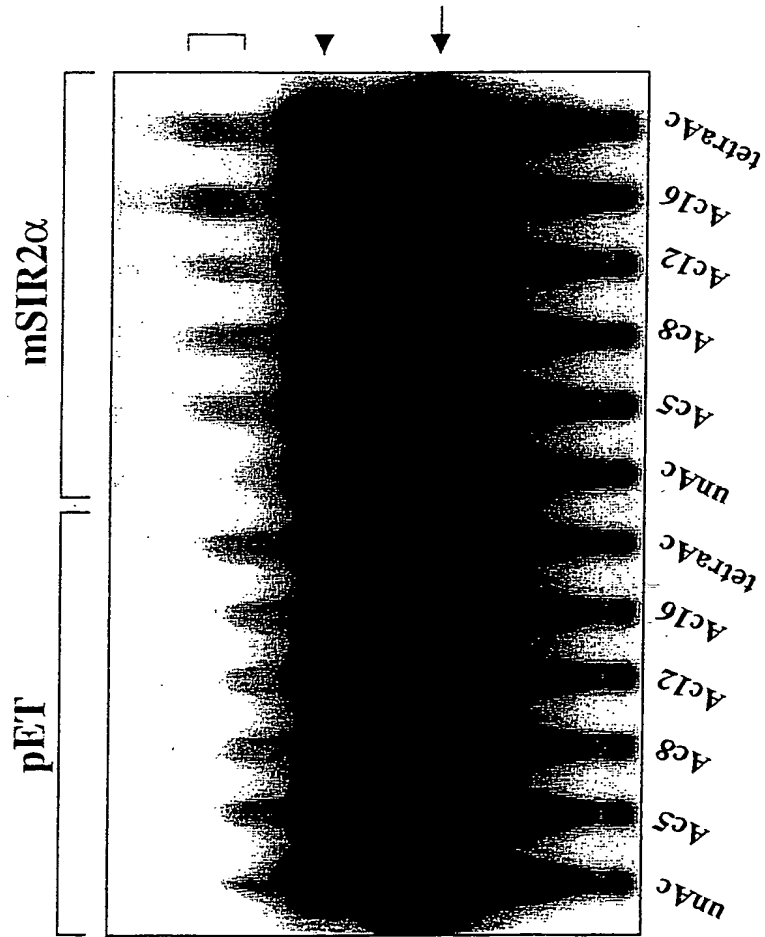


Figure 5C

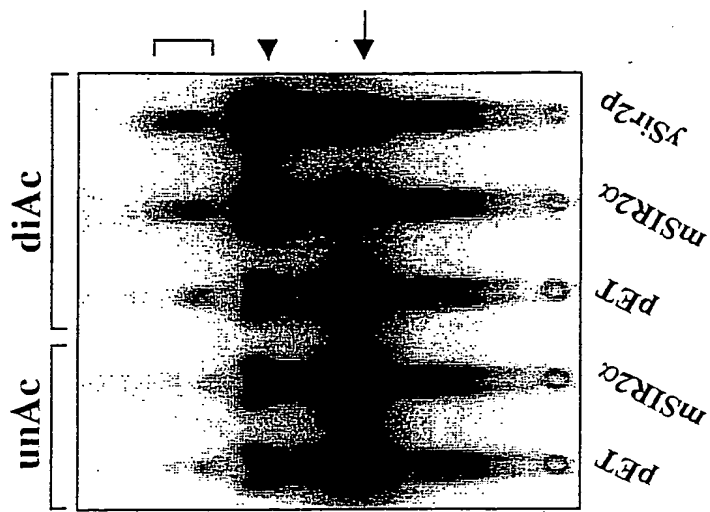


Figure 5B

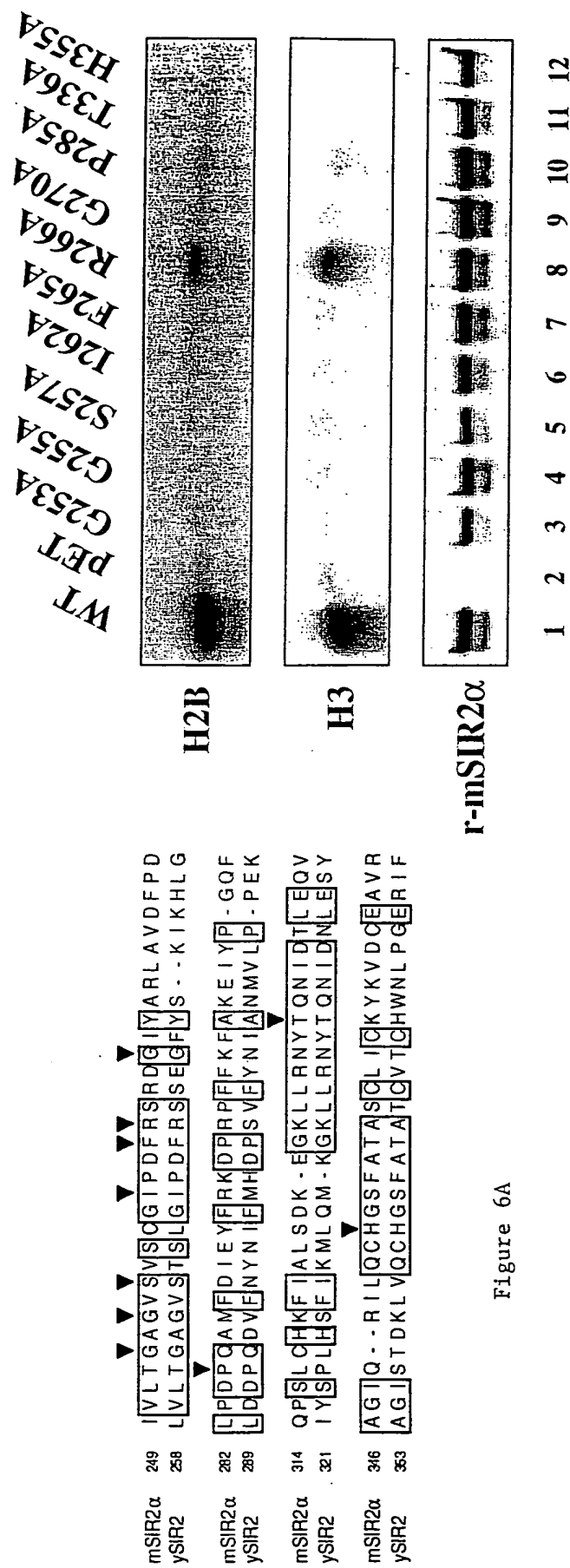


Figure 6A

Figure 6B

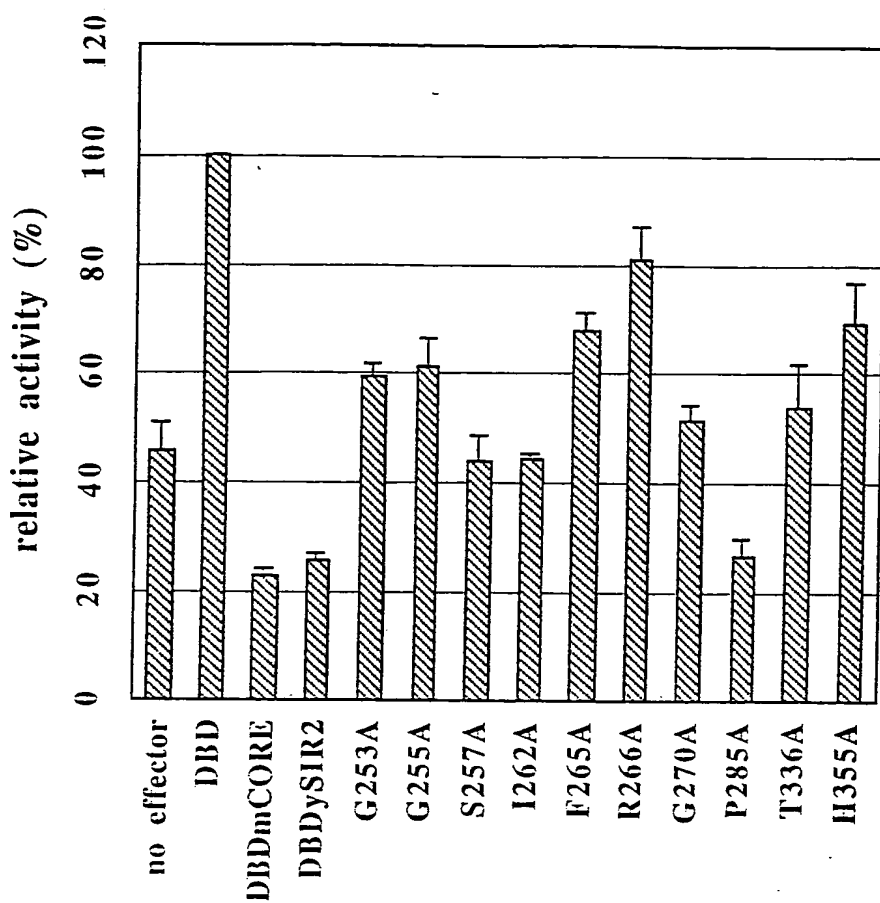


Figure 6D

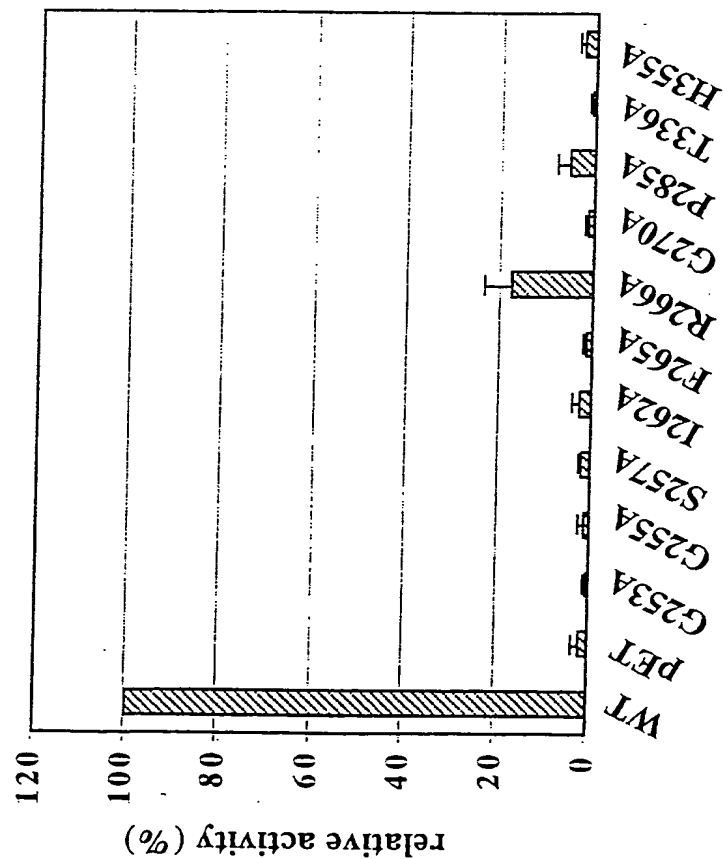


Figure 6C



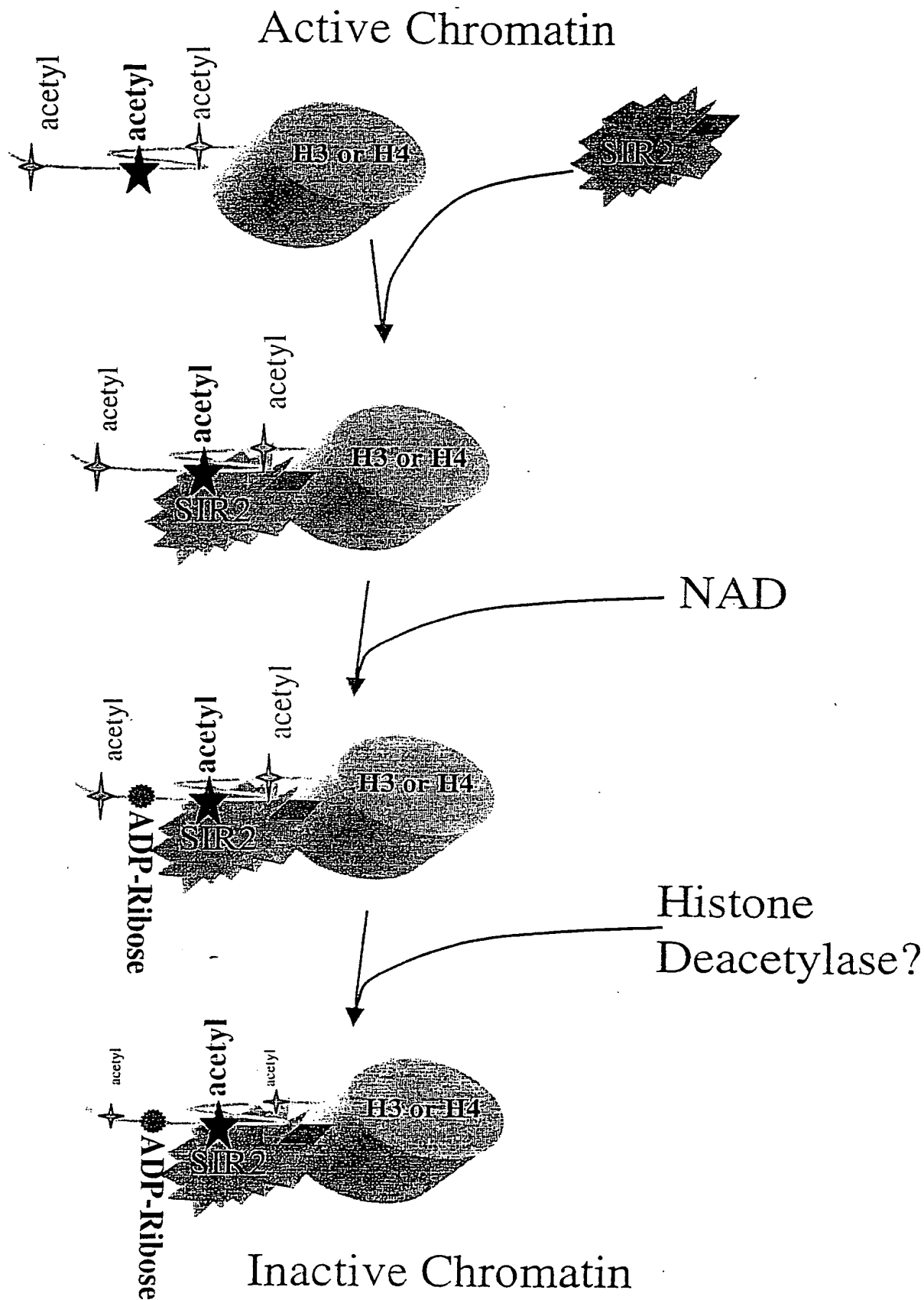


Figure 7

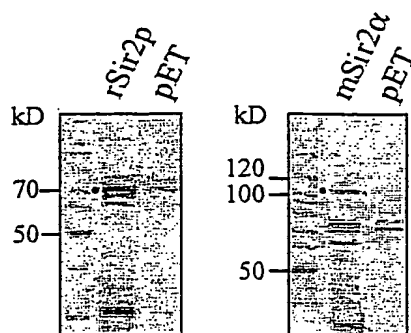


Figure 8a

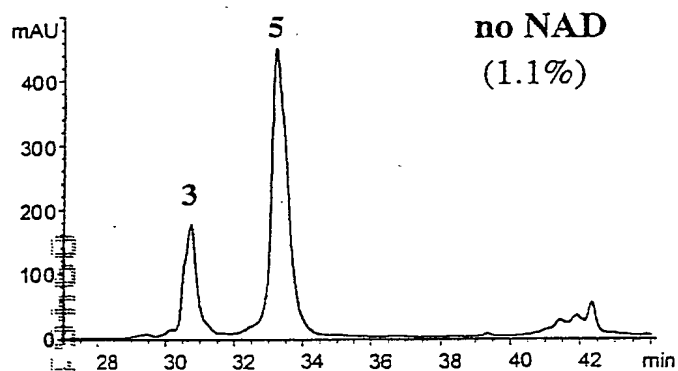


Figure 8b

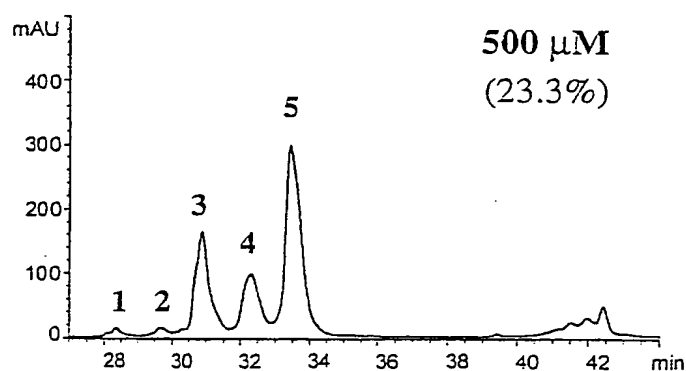


Figure 8e

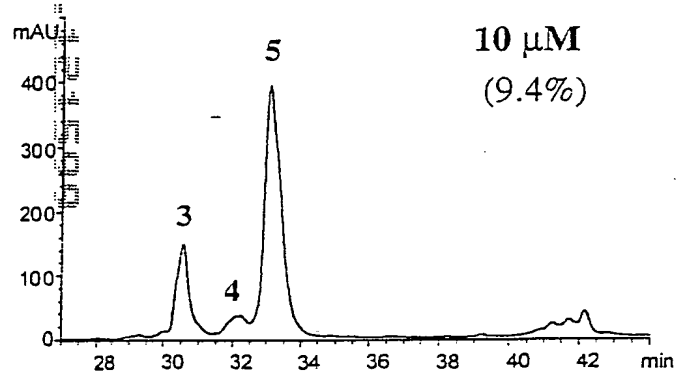


Figure 8c

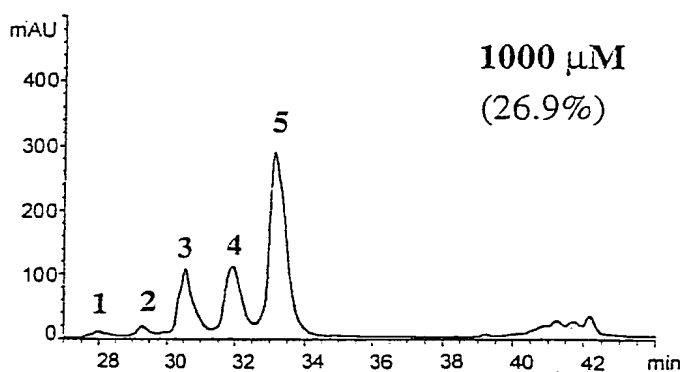


Figure 8f

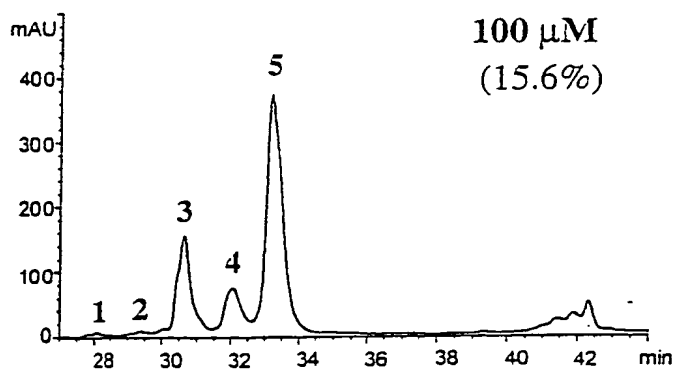


Figure 8d

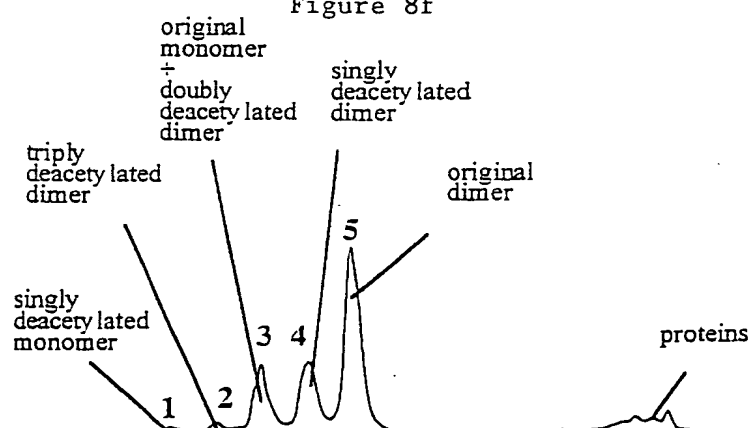


Figure 8g

Figure 9a

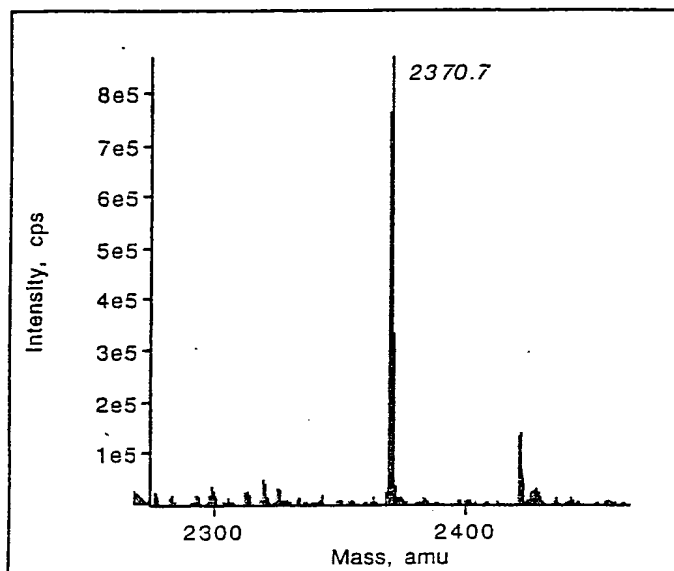


Figure 9b

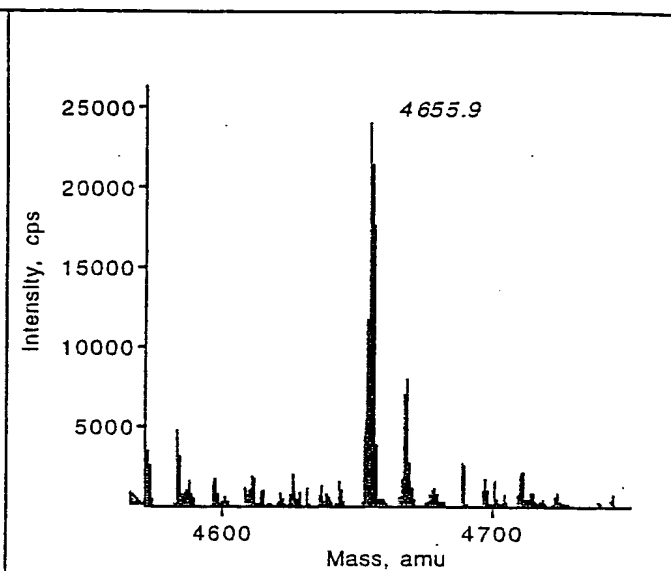


Figure 9c

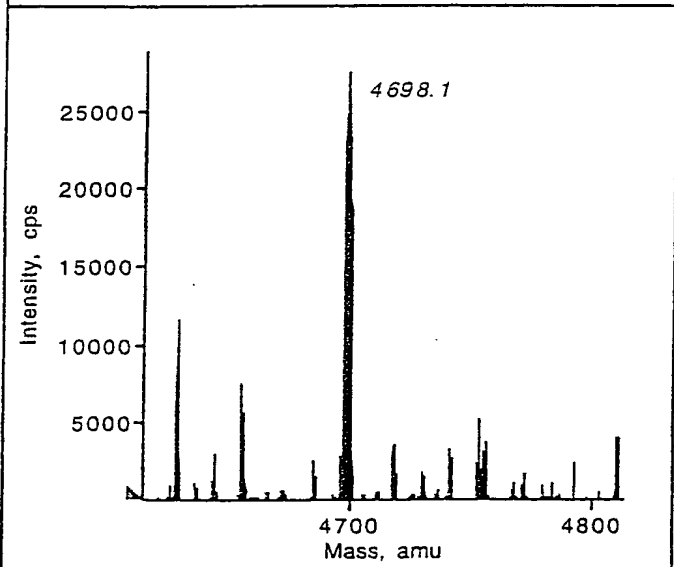
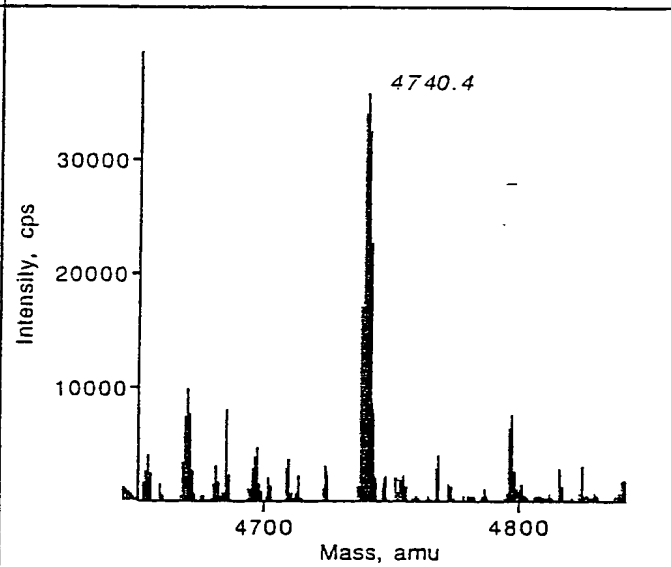


Figure 9d



## peak 4

## peak 5

9

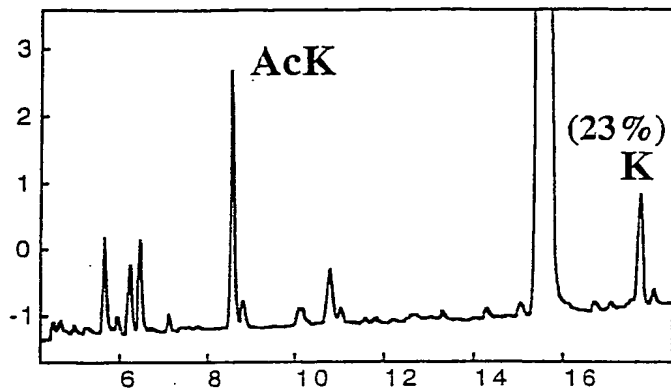


Figure 10a

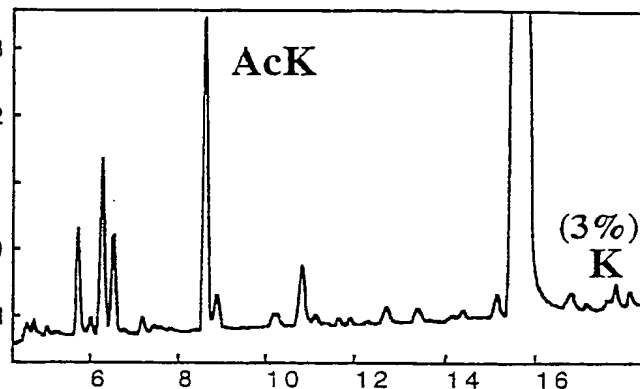


Figure 10d

14

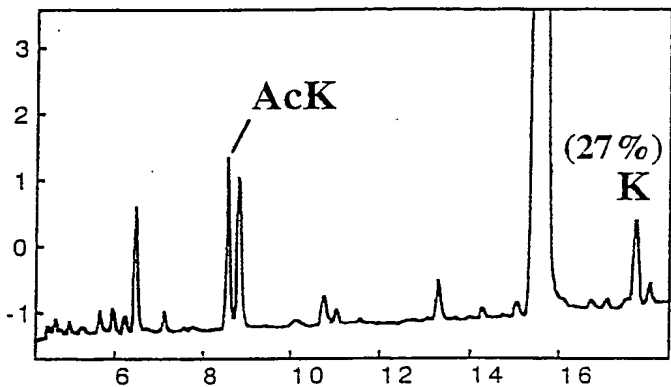


Figure 10b

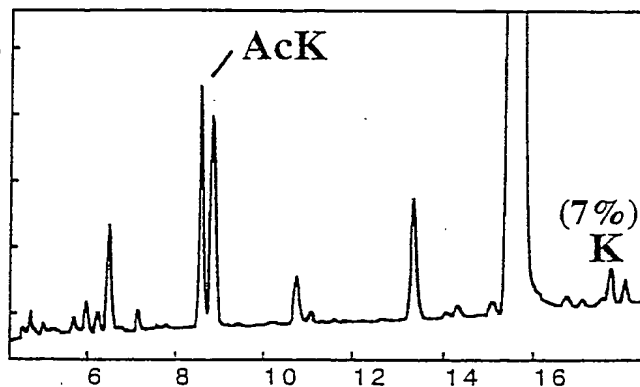


Figure 10e

18

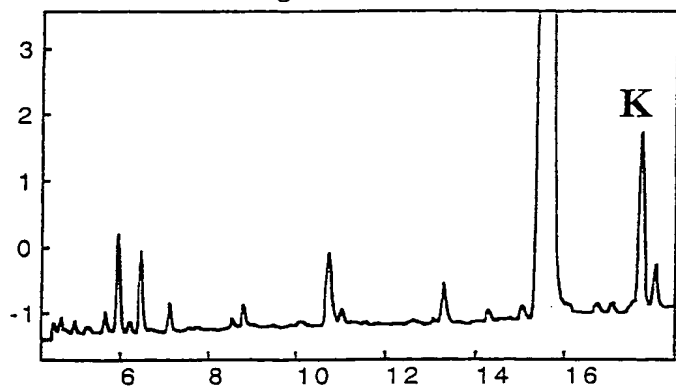


Figure 10c

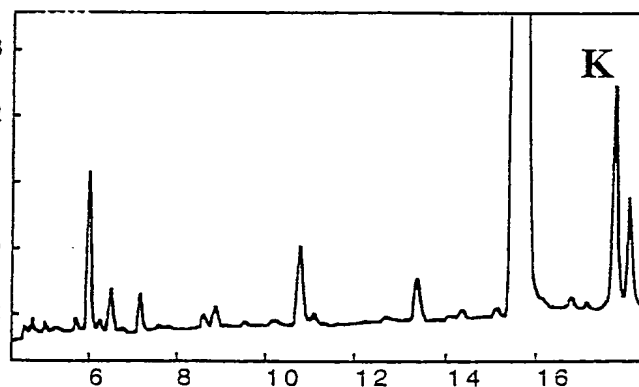


Figure 10f

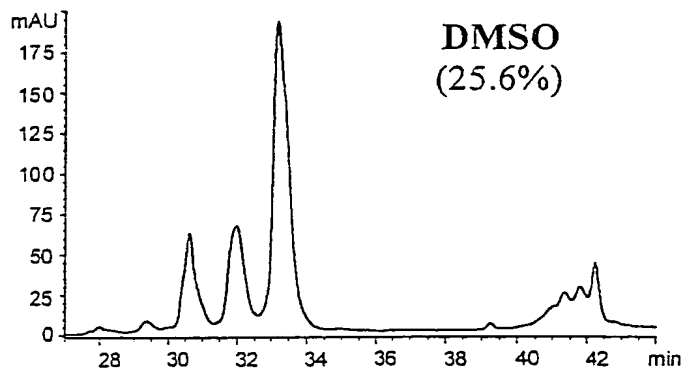


Figure 11a

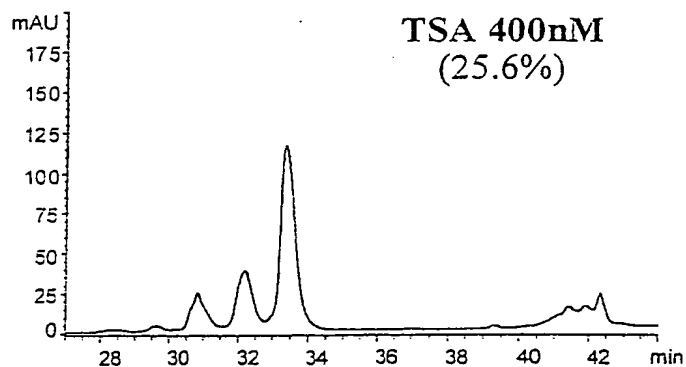


Figure 11b

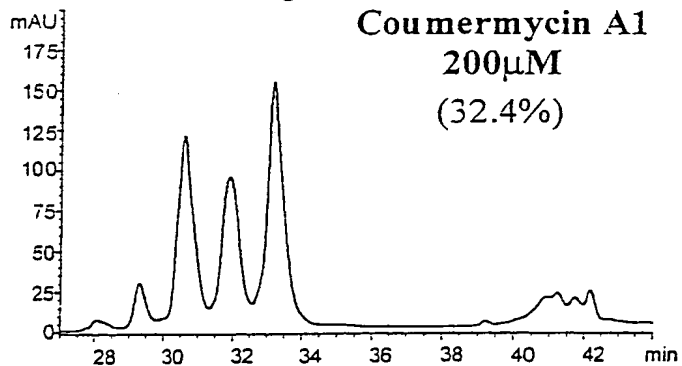


Figure 11e

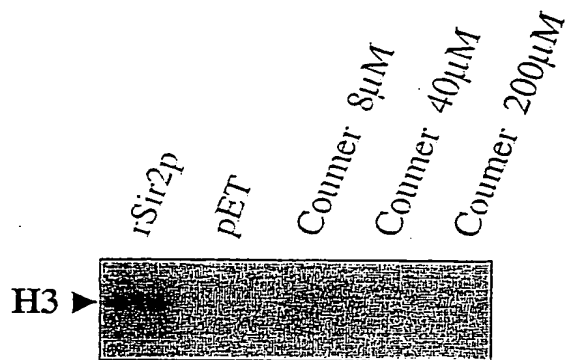


Figure 11c

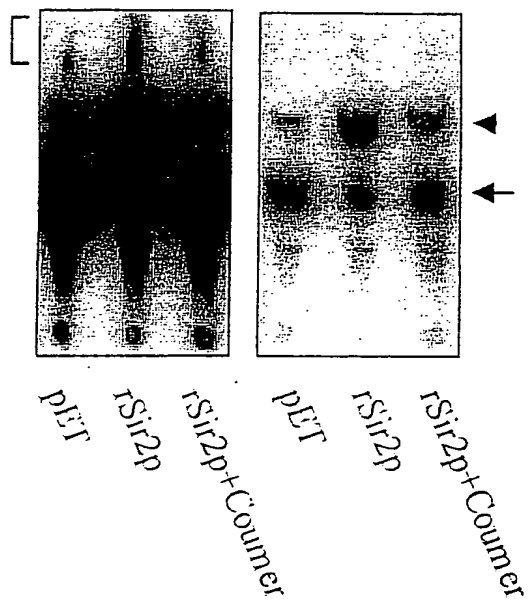


Figure 11d

1 MADEVALALQAAAGSPSAAAAAMEAASQPADEPLRKRRRRDG  
41 PGLGNPGEPAAVAPAAAGCEAASAAAPAAALWREAAGAA  
81 ASAREAPATAVAGDGNSSGLRRREPRAADDFFDDDEGE  
121 DEAAAAAIAIYRDNLITDGLLNGFHSCESSDDORT  
161 SHASSDWTTPRPRIGPYTFVQQHLMIGTDPRTILKDLLPE  
201 TIPPPELDDMTLWQIVINILSEPPKRRKRKDIINTIEDAYK  
241 LLOECKKIIIVLTGAGVSVSCGIPDFRSRDGIYARLAVDFP  
281 DLPDQAMFDIEYFRKDPFPFFKFAKEIYPGQFQPSLCHK  
321 FIALSDKEGKLLRNYTONIDTLEQVAGIQRI LQCHGSFAI  
361 ASCLICKYKYDCEAVRGOIFNQVVRCPRCPADEPLAIMK  
401 PEIVFFGENLPEQFHRAMKYDKDEVLLIVIGSSLKVRPV  
441 ALIPSSIPHEVPOILINREP LPHLHFDVE LLGDCDVIINE  
481 LCHRLGOEYAKLCCNPVKLSEITEKPPRPQKELVHLSLP  
521 PTPLHISEDSSSPERTVPQDSSVIATLVDQATNNVNDLE  
561 VSESSCVEEKPOEVQTSRNVENINVENPDFKAVGSSTADK  
601 NERTSVAETVRKCPNRLAKEQISKRLEGNOYLFVPPNRY  
641 IFHGAEVYSDSEDDVLSSSCGNSDSGTCSQSPSLEEPLE  
681 DESEIEEFYNGLEDTERPECAQGSFGADGGDQEVVNEA  
721 IATROELTDVNYPSDKS

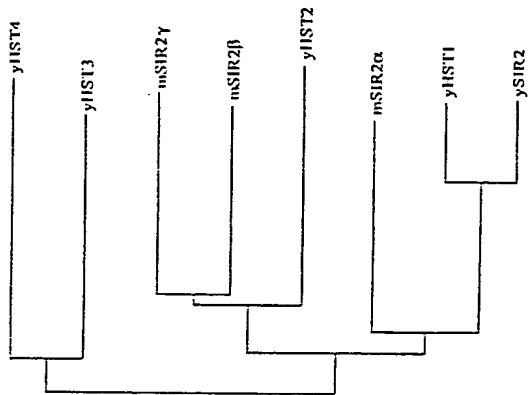


Figure 12a

Figure 12b

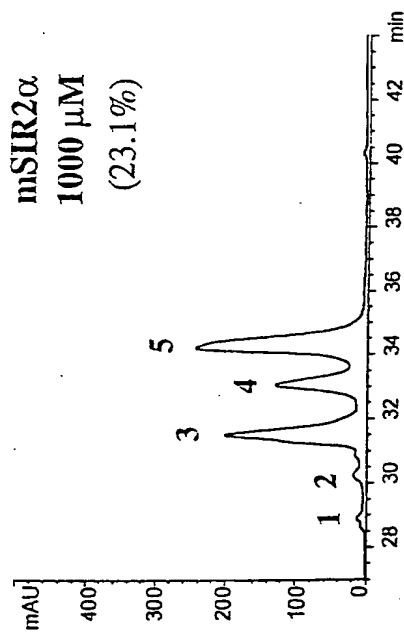


Figure 12c

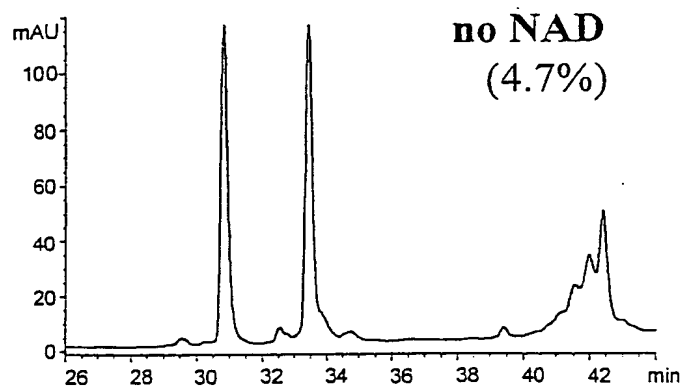


Figure 13a

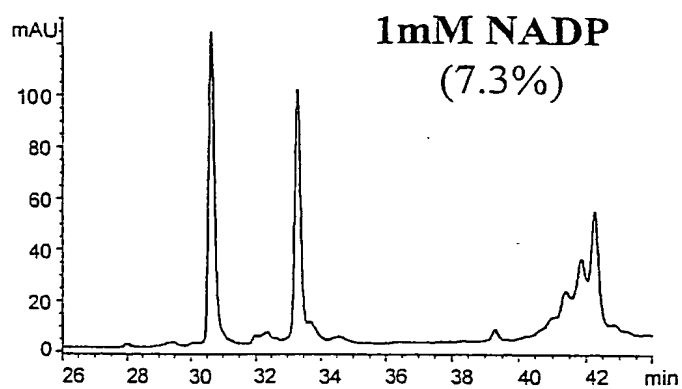


Figure 13d

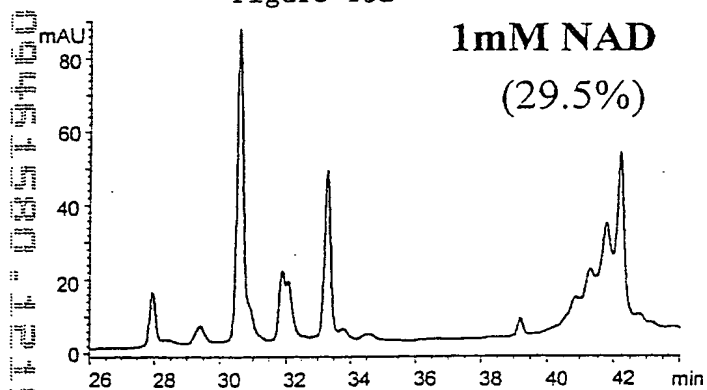


Figure 13b

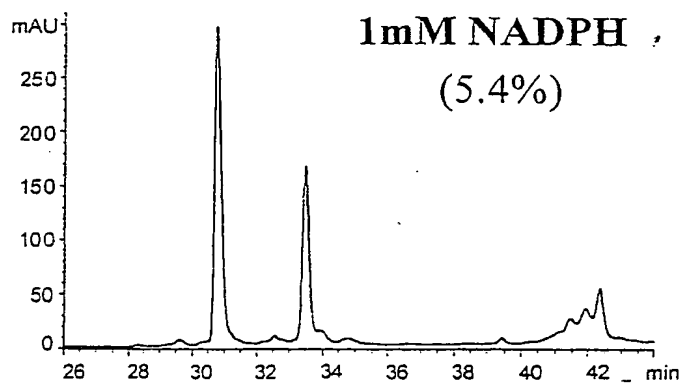


Figure 13e

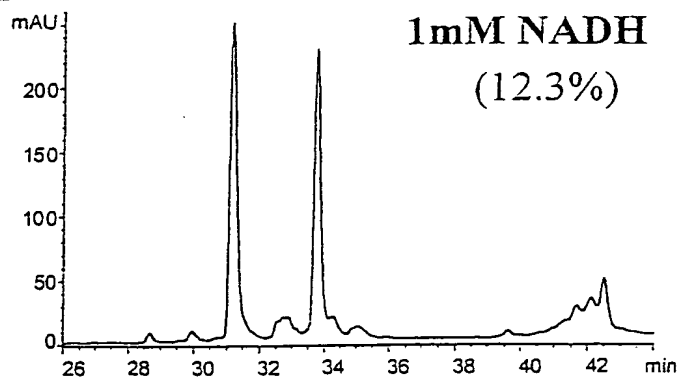


Figure 13c

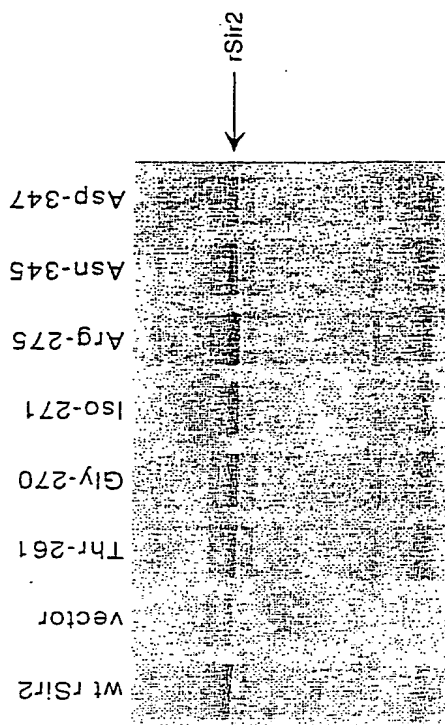
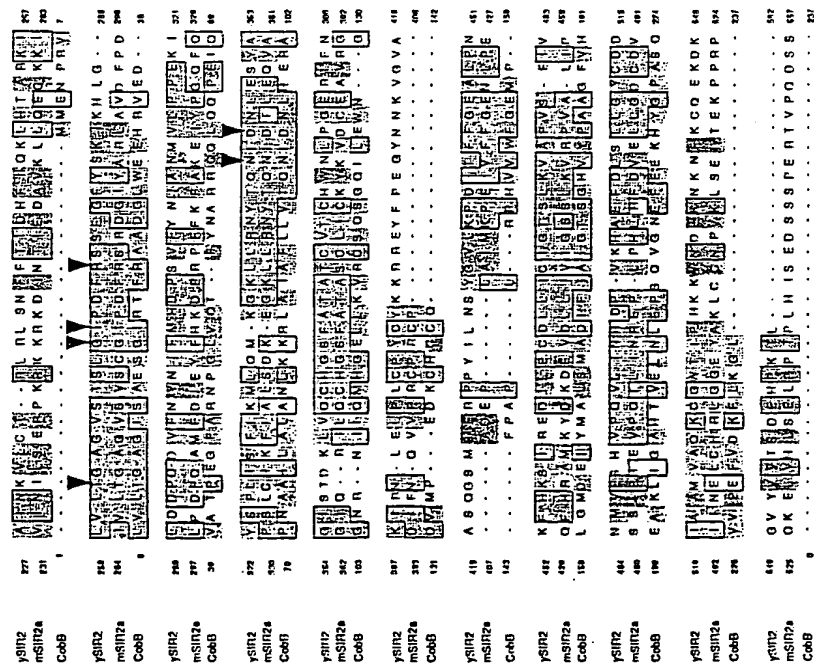


Figure 14b

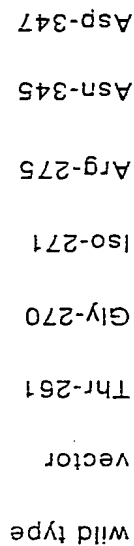


Figure 14c



Figure 14a



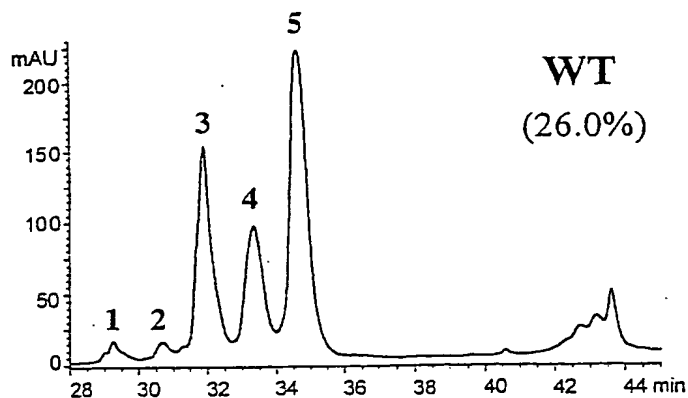


Figure 15a

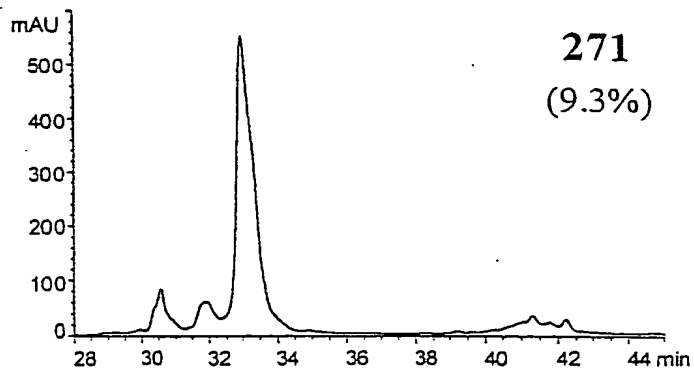


Figure 15e

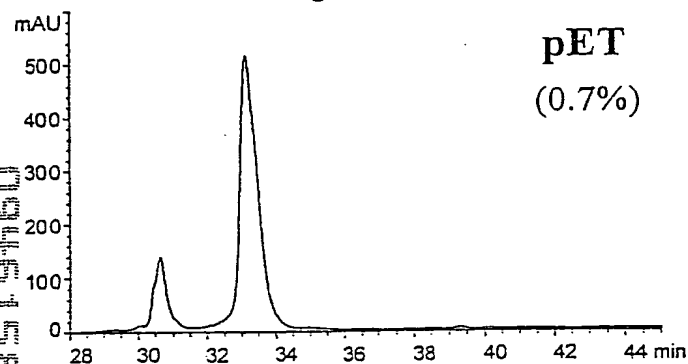


Figure 15b

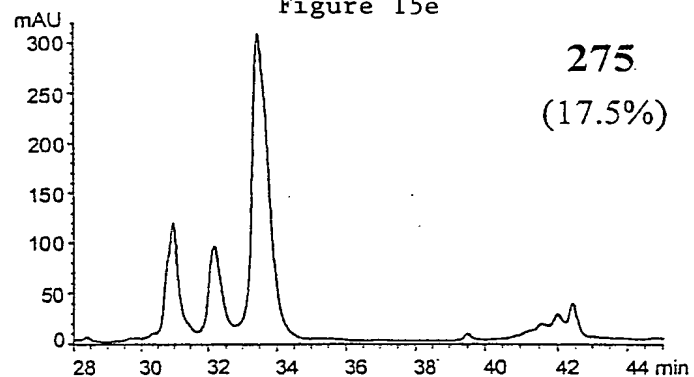


Figure 15f

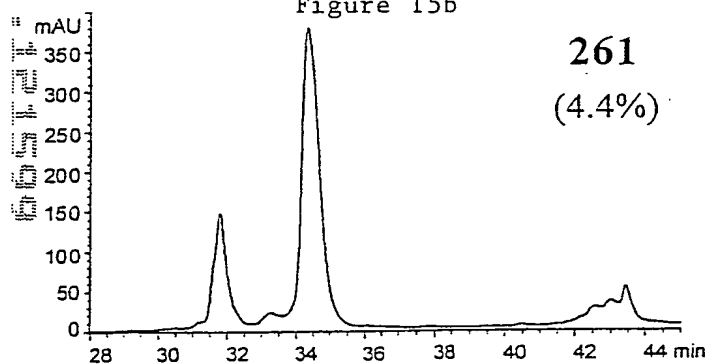


Figure 15c

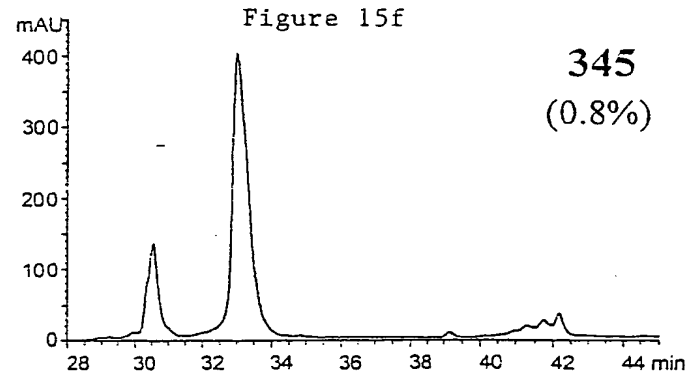


Figure 15g

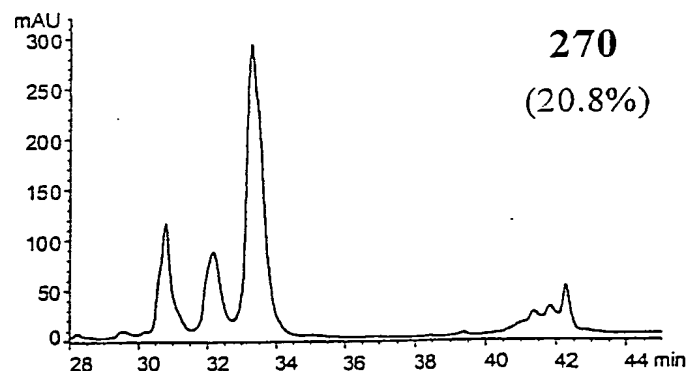


Figure 15d

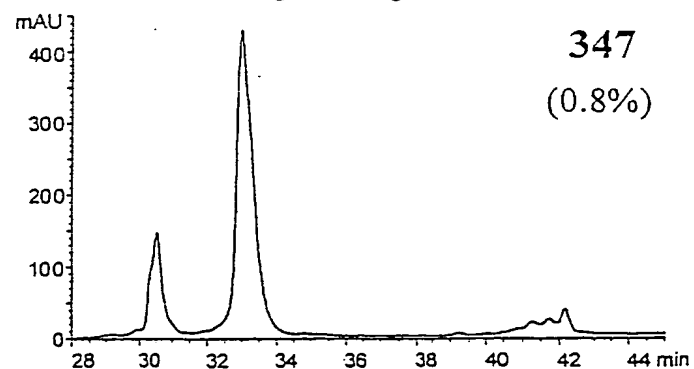


Figure 15h

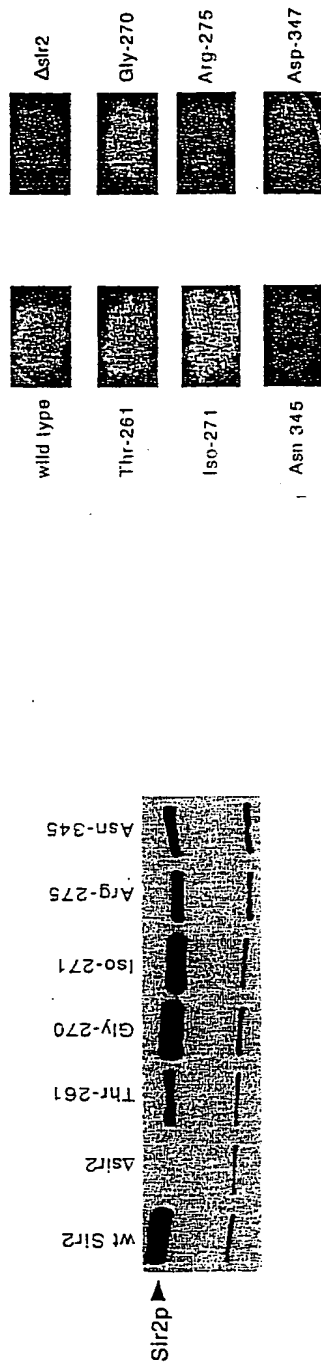


Figure 16a

Figure 16b

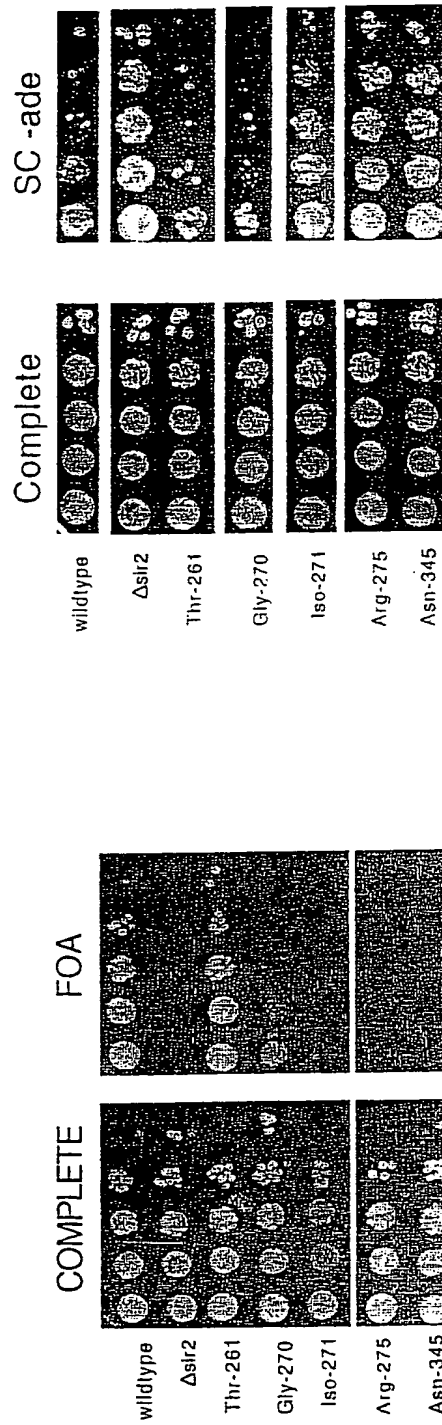


Figure 16c

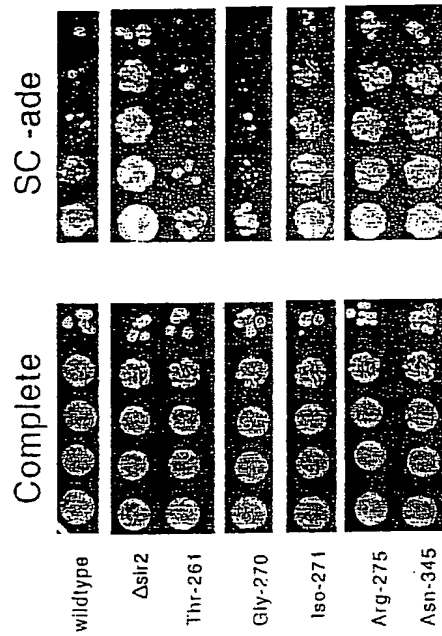


Figure 16d

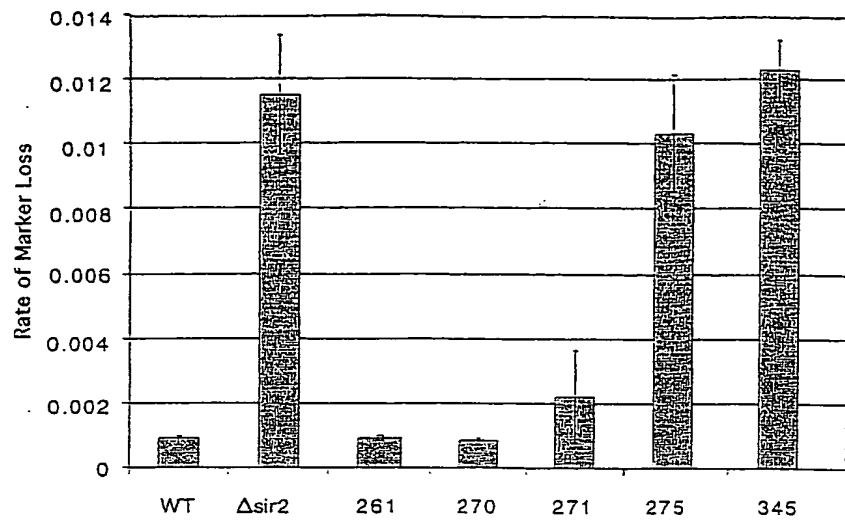


Figure 17a

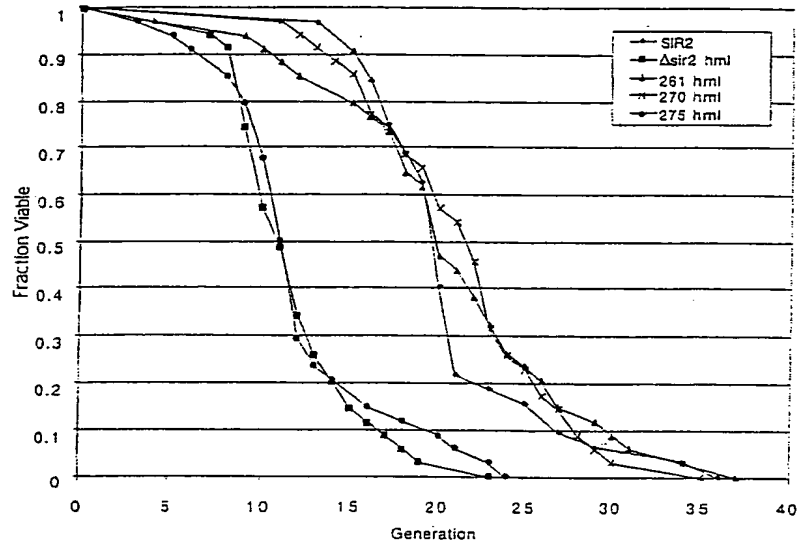


Figure 17b

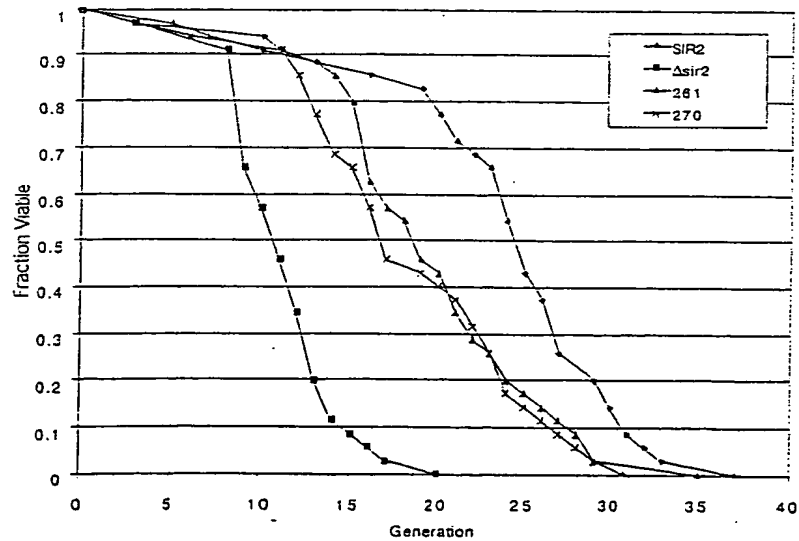


Figure 17c

| Mutant   | ADP-Rib. Activity (% of wt) | Deacetylase Activity (% of wt) | HM Silencing | Telomere Silencing | rDNA Silencing | rDNA Recombination | Mean Life Span (HML+) |
|----------|-----------------------------|--------------------------------|--------------|--------------------|----------------|--------------------|-----------------------|
| sir2Δ    | 0%                          | 2.7%                           | -            | -                  | -              | 1.15%              | 11.4                  |
| wildtype | 100%                        | 100%                           | +            | +                  | +              | 0.09%              | 24.4                  |
| Thr-261  | 4%                          | 17%                            | +            | +                  | +              | 0.09%              | 19.8                  |
| Gly-270  | 7%                          | 80%                            | +            | +/-                | +              | 0.08%              | 18.9                  |
| Iso-271  | 8%                          | 36%                            | +            | -                  | +/-            | 0.22%              | ND                    |
| Arg-275  | 100%                        | 67%                            | -            | -                  | -              | 1.03%              | ND                    |
| Asn-345  | 0%                          | 3%                             | -            | -                  | -              | 1.22%              | ND                    |
| Asp-347  | 0%                          | 3%                             | -            | ND                 | ND             | ND                 | ND                    |

Figure 18

|            |     |                        |   |               |   |     |
|------------|-----|------------------------|---|---------------|---|-----|
| ySIR2      | 257 | FLVLTGAGVSTSLGIPDFRS   | - | SEGFEYSKGRKH  | - | 286 |
| yHST1      | 203 | FLVLTGAGVSTSLGIPDFRS   | - | SEGFEYSKGRKH  | - | 232 |
| yHST2      | 27  | VLFMYGAGISTSCGIPDFRS   | P | GTGLYHNLAR    | - | 57  |
| yHST3      | 55  | IACLTGAGISCNAGIPDFRS   | - | SDGLYDLVKKDC  | - | 86  |
| yHST4      | 95  | MVVVSAGAGISVAAAGIPDFRS | - | SEGFEYSTVNGGS | - | 126 |
| mSIR2alpha | 263 | FLVLTGAGVSVSCGIPDFRS   | - | RIDGLYARLAVDF | - | 294 |
| mSIR2beta  | 79  | VIGLVGAGISTSAAGIPDFRS  | P | STGLYANLEK    | - | 109 |
| mSIR2g...  | 1   | -                      | - | GTRLYSNLQQ    | - | 10  |
| AI465098   | 48  | VVFHTGAGISTASGIPDFRC   | - | PHGVWTMEER    | - | 77  |
| AI465820   | 67  | LLVMTGAGISTESGLPDYRS   | E | KVGLYARTDR    | - | 97  |
| AI466061   | 59  | LAFTSGAGVSAESGVPTERC   | - | AGGYWRKWQA    | - | 88  |

|            |     |               |   |              |              |              |         |     |
|------------|-----|---------------|---|--------------|--------------|--------------|---------|-----|
| ySIR2      | 287 | -             | - | LGLDDPDQDVFN | NYNFMHDPSSV  | -            | FYNFANM | 314 |
| yHST1      | 233 | -             | - | LGLEDPQDVFN  | NLDIFLQDPSV  | -            | FYNFAHM | 260 |
| yHST2      | 58  | -             | - | LKLPPYEA     | VDVDFEQSDPLP | -            | FYTIAKE | 85  |
| yHST3      | 87  | SQYWSIKSGREME | D | ISLFRDDFKIS  | I            | FAKEMER      | 119     |     |
| yHST4      | 127 | -             | - | GKDLFDYNRY   | YGDESMSLKFN  | -            | QIMVSLF | 154 |
| mSIR2alpha | 295 | -             | - | PDLPDPQAV    | DEYFRKDP RP  | -            | EFKFAKE | 322 |
| mSIR2beta  | 110 | -             | - | YHLPYPEA     | EISYFKKHPEP  | -            | EFALAKE | 137 |
| mSIR2g...  | 11  | -             | - | YDLPYPEA     | ELGFFHNP KP  | -            | EFMLAKE | 38  |
| AI465098   | 78  | -             | - | GLAPKFDTE    | ENA          | -            | -       | 90  |
| AI465820   | 98  | -             | - | RPIQ         | -            | HIDFVPVLRASG | -       | 114 |
| AI466061   | 89  | -             | - | QDLATPQAFA   | RNPSQVWEFYH  | -            | YRRE    | 113 |

|            |     |     |           |           |               |              |         |        |        |
|------------|-----|-----|-----------|-----------|---------------|--------------|---------|--------|--------|
| ySIR2      | 315 | VLP | -         | PEK       | YSPL          | HSFKMLQMKGK  | LE      | RNYTON | 345    |
| yHST1      | 261 | VLP | -         | PE        | NMYSPL        | HSFKMLQDKGK  | LE      | RNYTON | 291    |
| yHST2      | 86  | LYP | -         | GNFRPSKE  | HYLLKLFQDKDV  | LE           | KPVYTON | 116    |        |
| yHST3      | 120 | LYS | NVQLAKPTK | TH        | KFAHDKDRNK    | LE           | KPCYTON | 152    |        |
| yHST4      | 155 | RLS | -         | KNCQPTK   | THEMLNEFARDGR | LE           | BLYTON  | 185    |        |
| mSIR2alpha | 323 | LYP | -         | GQFQPSL   | GHKFI         | ALS          | DKGK    | LE     | RNYTON |
| mSIR2beta  | 138 | LYP | -         | GQFKPTIC  | HYF           | RLLKEKGL     | LE      | RCYTON | 168    |
| mSIR2g...  | 39  | LYP | -         | CHYRPNVTH | YFL           | RLLHDKEL     | LE      | RLYTON | 69     |
| AI465098   | 91  | -   | -         | R         | PSKTH         | MAV          | LERMGF  | LS     | FLVSON |
| AI465820   | 115 | TWP | -         | ENLWAG    | LN            | SPLTNPTQHTWL | -       | -      | 137    |
| AI466061   | 114 | VMR | -         | SK        | EPNPGHLA      | AQCEAR       | -       | -      | 133    |

|            |     |     |            |      |                    |   |   |   |           |     |
|------------|-----|-----|------------|------|--------------------|---|---|---|-----------|-----|
| ySIR2      | 346 | IDN | LESYAGIS   | STD  | -                  | - | - | - | KLVO      | 362 |
| yHST1      | 292 | IDN | LESYAGI    | DRD  | -                  | - | - | - | KLVO      | 308 |
| yHST2      | 117 | IDT | LERQAGV    | KDD  | -                  | - | - | - | LEIE      | 133 |
| yHST3      | 153 | IDG | LEES       | GLT  | LSNRKLPLTSFSSHWKNL | - | - | - | DVVQ      | 185 |
| yHST4      | 186 | IDG | LDLQILPHLS | TN   | -                  | - | - | - | VPLAKPIPS | 211 |
| mSIR2alpha | 354 | IDT | LEQVAGI    | QR   | -                  | - | - | - | ILQ       | 368 |
| mSIR2beta  | 169 | IDT | LERVAGL    | EPQ  | -                  | - | - | - | DLVE      | 185 |
| mSIR2g...  | 70  | IDG | LERASG     | PAS  | -                  | - | - | - | KLVE      | 86  |
| AI465098   | 116 | VDG | LDLVRS     | GFRD | -                  | - | - | - | KLAE      | 132 |
| AI465820   | 0   | -   | -          | -    | -                  | - | - | - | -         | 137 |
| AI466061   | 0   | -   | -          | -    | -                  | - | - | - | -         | 133 |

Figure 19

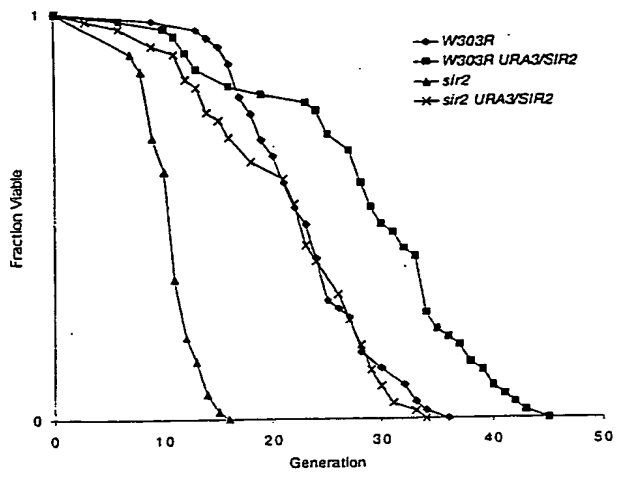


Figure 20

10 20 30 40 50 60  
 GCGGAGCAGAGGAGGCGAGGCGGAGGCGCCAGAGAGGCAGTTGGAAGATGGCGGACGAGG  
 M A D E V

70 80 90 100 110 120  
 TGGCGCTCGCCCTTCAGGCCGCCGGCTCCCCCTTCGCGGGCGGCCGCCATGGAGGCCGCGT  
 A L A L Q A A G S P S A A A A M E A A S

130 140 150 160 170 180  
 CGCAGCCGGCGGACGAGCCGCTCCGCAAGAGGCCCGCCGAGACGGGCCTGGCCTCGGGC  
 Q P A D E P L R K R P R R D G P G L G R

190 200 210 220 230 240  
 GCAGCCCGGGCGAGCCGAGCGCAGCAGTGGCGCCGGCGGCCGCGGGGTGTGAGGCGGCGA  
 S P G E P S A A V A P A A A G C E A A S

250 260 270 280 290 300  
 GCGCCGCGGCCCCCGCGGCGCTGTGGCGGGAGGCGGCAGGGGCGGCGGCGAGCGCGGAGC  
 A A A P A A L W R E A A G A A A S A E R

310 320 330 340 350 360  
 GCGAGGCCCGGCGGACGGCCGTGGCCGGGGACGGAGACAATGGGTCCGGCCTGCGGCGGG  
 E A P A T A V A G D G D N G S G L R R E

370 380 390 400 410 420  
 AGCCGAGGGCGGCTGACGACTTCGACGACGACGAGGGCGAGGAGGAGACGAGGCGGCGG  
 P R A A D D F D D D E G E E E D E A A A

430 440 450 460 470 480  
 CGGCAGCGGCGGCGGCGAGCGATCGGCTACCGAGACAACCTCCTGTTGACCGATGGACTCC  
 A A A A A A I G Y R D N L L L T D G L L

490 500 510 520 530 540  
 TGAATAATGGCTTTTCATTCTGTGAAAGTGATGACGATGACAGAACGTCACACGCCAGCT  
 T N G F H S C E S D D D D R T S H A S S

550 560 570 580 590 600  
 CTAGTGACTGGACTCCGCGGCCGCGGATAGGTCCATATACTTTTGTTCAGCAACATCTCA  
 S D W T P R P R I G P Y T F V Q Q H L M

610 620 630 640 650 660  
 TGATTGGCACCGATCCTCGAACAATTCTTAAAGATTTTATTACCAGAAACAATTCTCCAC  
 I G T D P R T I L K D L L P E T I P P P

670 680 690 700 710 720  
 CTGAGCTGGATGATATGACGCTGTGGCAGATTGTTATTAAATATCCTTTCAGAACCACCAA  
 E L D D M T L W Q I V I N I L S E P P K

730 740 750 760 770 780  
 AGCGGAAAAAAGAAAAGATATCAATACAATTGAAGATGCTGTGAAGTTACTGCAGGAGT  
 R K K R K D I N T I E D A V K L L Q E C

790 800 810 820 830 840  
 GTAAAAAGATAATAGTTCTGACTGGAGCTGGGGTTTCTGTCTCCTGTGGGATTCTGACT  
 K K I I V L T G A G V S V S C G I P D F

850 860 870 880 890 900  
 TCAGATCAAGAGACGGTATCTATGCTCGCCTTGCGGTGGACTTCCCAGACCTCCCAGACC  
 R S R D G I Y A R L A V D F P D L P D P

Figure 21 a

910 920 930 940 950 960  
 CTCAAGCCATGTTTGTATATTGAGTATTTTAAAGACCCAAGACCATTCTTCAAGTTTG  
 Q A M F D I E Y F K D P R P F F K F A

970 980 990 1000 1010 1020  
 CAAAGGAAATATATCCCGACAGTTCCAGCCGTCTCTGTGTACAAATTCATAGCTTTGT  
 K E I Y P G Q F Q P S L C H K F I A L S

1030 1040 1050 1060 1070 1080  
 CAGATAAGGAAGGAAAACCTACTTCGAAATTATACTCAAAAATATAGATACCTTGGAGCAGG  
 D K E G K L L R N Y T Q N I D T L E Q V

1090 1100 1110 1120 1130 1140  
 TTGCAGGAATCCAAAGGATCCTTCAGTGTTCATGGTTCTTTGCAACAGCATCTTGCCTGA  
 A G I Q R I L Q C H G S F A T A S C L I

1150 1160 1170 1180 1190 1200  
 TTTGTAAATACAAAGTTGATTGTGAAGCTGTTTCGTGGAGACATTTTAAATCAGGTAGTTC  
 C K Y K V D C E A V R G D I F N Q V V P

1210 1220 1230 1240 1250 1260  
 CTCGGTGGCCTAGGTGCCCAGCTGATGAGCCACTTGCCATCATGAAGCCAGAGATTGTCT  
 R C P R C P A D E P L A I M K P E I V F

1270 1280 1290 1300 1310 1320  
 TCTTTGGTGAAAACCTTACCAGAACAGTTTTCATAGAGCCATGAAGTATGACAAAGATGAAG  
 F G E N L P E Q F H R A M K Y D K D E V

1330 1340 1350 1360 1370 1380  
 TTGACCTCCTCATTTGTTATTGGATCTTCTCTGAAAGTGAGACCAGTAGCACTAATTCCAA  
 D L L I V I G S S L K V R P V A L I P S

1390 1400 1410 1420 1430 1440  
 GTTCTATACCCCATGAAGTGCCTCAAATATTAATAAATAGGGAACCTTTGCCTCATCTAC  
 S I P H E V P Q I L I N R E P L P H L H

1450 1460 1470 1480 1490 1500  
 ATTTTGTAGTAGAGCTCCTTGGAGACTGCGATGTTTATAATTAATGAGTTGTGTTCATAGGC  
 F D V E L L G D C D V I I N E L C H R L

1510 1520 1530 1540 1550 1560  
 TAGGTGGTGAATATGCCAAACTTTGTTGTAACCCTGTAAAGCTTTCAGAAATTACTGAAA  
 G G E Y A K L C C N P V K L S E I T E K

1570 1580 1590 1600 1610 1620  
 AACCTCCACGCCCAAAAAGGAATTGGTTCAATTTATCAGAGTTGCCACCAACACCTCTTC  
 P P R P Q K E L V H L S E L P P T P L H

1630 1640 1650 1660 1670 1680  
 ATATTTTCGGAAGACTCAAGTTTCACCTGAAAGAACTGTACCACAAGACTCTTCTGTGATTG  
 I S E D S S S P E R T V P Q D S S V I A

1690 1700 1710 1720 1730 1740  
 CTACACTTGTAGACCAAGCAACAACAATGTTAATGATTTAGAAGTATCTGAATCAA  
 T L V D Q A T N N N V N D L E V S E S S

1750 1760 1770 1780 1790 1800  
 GTTGTGTGGAAGAAAAACCACAAGAAGTACAGACTAGTAGGAATGTTGAGAACATTAAATG  
 C V E E K P Q E V Q T S R N V E N I N V

1810 1820 1830 1840 1850 1860  
 TGGAAAATCCAGATTTTAAAGGCTGTTGGTTCCAGTACTGCAGACAAAAATGAAAGAACTT  
 E N P D F K A V G S S T A D K N E R T S

1870 1880 1890 1900 1910 1920  
 CAGTTGCAGAAACAGTGAGAAAATGCTGGCCTAATAGACTTGCAAAGGAGCAGATTAGTA  
 V A E T V R K C W P N R L A K E Q I S K

Figure 21b



1930 1940 1950 1960 1970 1980  
 AGCGGCTTGAGGGTAATCAATACCTGTTTACCAAATCGTTACATATTCCACGGTG  
 R L E G N Q Y L F V P P N R Y I F H G A

1990 2000 2010 2020 2030 2040  
 CTGAGGTATACTCAGACTCTGAAGATGACGCTTTGTCTCTAGTTCTGTGGCAGTAACA  
 E V Y S D S E D D V L S S S S C G S N S

2050 2060 2070 2080 2090 2100  
 GTGACAGTGGCACATGCCAGAGTCCAAGTTTAGAAGAACCCTTGGAAGATGAAAGTGAAA  
 D S G T C Q S P S L E E P L E D E S E I

2110 2120 2130 2140 2150 2160  
 TTGAAGAATTCTACAATGGCTTGGAAGATGATACGGAGAGGCCCGAATGTGCTGGAGGAT  
 E E F Y N G L E D D T E R P E C A G G S

2170 2180 2190 2200 2210 2220  
 CTGGATTTGGAGCTGATGGAGGGGATCAAGAGGTTGTTAATGAAGCTATAGCTACAAGAC  
 G F G A D G G D Q E V V N E A I A T R Q

2230 2240 2250 2260 2270 2280  
 AGGAATTGACAGATGTAACTATCCATCAGACAAATCATAACACTATTGAAGCTGTCCGG  
 E L T D V N Y P S D K S \*

2290 2300 2310 2320 2330 2340  
 ATTCAGGAATTGCTCCACCAGCATTTGGGAACTTTAGCATGTCAAAAAATGAATGTTTAC

2350 2360 2370 2380 2390 2400  
 TTCTGAACTTGAACAAGGAAATCTGAAAGATGTATTATTTATAGACTGGAAAATAGATTG

2410 2420 2430 2440 2450 2460  
 TCTTCTTGATAATTTCTAAAGTTCCATCATTTCTGTTTGTACTTGTACATTCAACACTG

2470 2480 2490 2500 2510 2520  
 TTGGTTGACTTCATCTTCTTCAAGGTTTCATTTGTATGATACATTCTGTATGTATGTATA

2530 2540 2550 2560 2570 2580  
 ATTTTGTTTTTTGCCTAATGAGTTTCAACCTTTTAAAGTTTCAAAGCCATTGGAATGT

2590 2600 2610 2620 2630 2640  
 TAAATGTAAAGGGAACAGCTTATCTAGACCAAAGAATGGTATTTACACTTTTTTGTGTTGT

2650 2660 2670 2680 2690 2700  
 AACATTGAATAGTTTAAAGCCCTCAATTTCTGTTCTGCTGAACTTTTATTTTAGGACAG

2710 2720 2730 2740 2750 2760  
 TTAACTTTTTAAACACTGGCATTTTCCAAAACCTTGTGGCAGCTAACTTTTTTAAATCACA

2770 2780 2790 2800 2810 2820  
 GATGACTTGTAATGTGAGGAGTCAGCACCGTGTCTGGAGCACTCAAACCTGGGCTCAGT

2830 2840 2850 2860 2870 2880  
 GTGTGAAGCGTACTTACTGCATCGTTTTTGTACTTGTCTGCAGACGTGGTAATGTCCAAAC

2890 2900 2910 2920 2930 2940  
 AGGCCCCTGAGACTAATCTGATAAATGATTTGGAAATGTGTTTCAGTTGTTCTAGAAACA

2950 2960 2970 2980 2990 3000  
 ATAGTGCCTGTCTATATAGGTCCCCCTTAGTTTGAATATTTGCCATTGTTTAATTAAATAC

3010 3020 3030 3040 3050 3060  
 CTATCACTGTGGTAGAGCCTGCATAGATCTTCACCACAAATACTGCCAAGATGTGAATAT

3070 3080 3090 3100 3110 3120  
 GCAAAGCCTTTCTGAATCTAATAATGGTACTTCTACTGGGGAGAGTGAATATTTTGGAC

3130 3140 3150 3160 3170 3180  
 TGCTGTTTTTCCATTAAATGAGGAAAGCAATAGGCCTCTTAATTAAAGTCCCAAAGTCATA

Figure 2lc

3190 3200 3210 3220 3230 3240  
 AGATAAATTGTAGCTCAACCAGAAAGTACACGTTGCCTGTTGAGGATTTGGTGTAAATGT  
 3250 3260 3270 3280 3290 3300  
 ATCCCAAGGTGTTAGCCTTGTATTATGGAGATGAATACAGATCCAATAGTCAAATGAAAC  
 3310 3320 3330 3340 3350 3360  
 TAGTTCTTAGTTATTTAAAAGCTTAGCTTGCCCTTAAAACTAGGGATCAATTTTCTCAACT  
 3370 3380 3390 3400 3410 3420  
 GCAGAACTTTTAGCCTTTCAAACAGTTACACACCTCAGAAAGTCAGTATTTATTTTACAG  
 3430 3440 3450 3460 3470 3480  
 ACTTCTTTGGAACATTGCCCCCAAATTTAAATATTCATGTGGGTTTAGTATTTATTACAA  
 3490 3500 3510 3520 3530 3540  
 AAAAATGATTTGAAATATAGCTGTTCTTTATGCATAAAATACCCAGTTAGGACCATTACT  
 3550 3560 3570 3580 3590 3600  
 GCCAGAGGAGAAAAGTATTAAGTAGCTCATTTCCCTACCTAAAAGATAACTGAATTTATT  
 3610 3620 3630 3640 3650 3660  
 TGGCTACACTAAAGAATGCAGTATATTTAGTTTTTCCATTTGCATGATGTGTTGTGCTAT  
 3670 3680 3690 3700 3710 3720  
 AGACAATATTTTAAATTGAAAAATTTGTTTTTAAATTATTTTTTACAGTGAAGACTGTTTTT  
 3730 3740 3750 3760 3770 3780  
 AGCTCTTTTTTATATTGTACATAGACTTTTATGTAATCTGGCATATGTTTTGTAGACCGTT  
 3790 3800 3810 3820 3830 3840  
 TAAATGACTGGATTATCTTCCTCCAACCTTTGAAATACAAAAACAGTGTTTTATACTAAAA  
 3850 3860 3870  
 AAAAAAAGTCGACGCGGCCCGCAATTC

Figure 2ld

10 20 30 40 50 60  
 CCACGCGTCCGCGGACGCGTGGGCACGGGACAGAGCAGTCGGTGACAGTCCCGAGGGCCC  
 T R P R T R G H G T E Q S V T V P R A P

70 80 90 100 110 120  
 CCACCCCGTTCCCATGGCCGAGCCGGACCGATTTCAGACTCGGACACTGAGGGAGGAGCCA  
 T P F P W P S R T D S D S D T E G G A T

130 140 150 160 170 180  
 CTGGTGAGAGGCAGAGATGGACTTCCTGAGGAATTTATTACCCAGACCCTGGGCCTGG  
 G G E A E M D F L R N L F T Q T L G L G

190 200 210 220 230 240  
 GTCCCAAAAGGAGCGTCTTCTAGACGAGCTGACCCTCGAAGGAGTGACACGCTACATGC  
 S Q K E R L L D E L T L E G V T R Y M Q

250 260 270 280 290 300  
 AGAGCGAGCGCTGCCGCAAGGTCATCTGTTTGGTGGGAGCCGGAATCTCCACGTCCGCGG  
 S E R C R K V I C L V G A G I S T S A G

310 320 330 340 350 360  
 GTATCCCTGACTTCCGCTCCCCGTCCTGACCTGACCTGCTATGCAAACCTGGAGAAGTACCACC  
 I P D F R S P S T G L Y A N L E K Y H L

370 380 390 400 410 420  
 TTCTTACCCAGAGGCCATCTTTGAGATCAGCTACTTCAAGAAACATCCGGAACCCTTCT  
 P Y P E A I F E I S Y F K K H P E P F F

430 440 450 460 470 480  
 TTGCCCTTGCCAAGGAGCTCTATCCCGGGCAGTTCAAGCCAACCATCTGCCACTACTTCA  
 A L A K E L Y P G Q F K P T I C H Y F I

490 500 510 520 530 540  
 TCCGCCTGCTGAAGGAGAAGGGGCTGCTGCTGCGCTGCTACACGCAGAACATAGACACGC  
 R L L K E K G L L L R C Y T Q N I D T L

550 560 570 580 590 600  
 TGGAACGAGTGGCGGGGCTGGAGCCCCAGGACCTGGTGGAGGCCACGGCACCTTCTACA  
 E R V A G L E P Q D L V E A H G T F Y T

610 620 630 640 650 660  
 CATCACTGTGTCAACACCTCCTGCAGAAAAGAATACACGATGGGCTGGATGAAAGAGA  
 S H C V N T S C R K E Y T M G W M K E K

670 680 690 700  
 AGATTTCTCAGAAGCAACTCCCAGGTGTGAGCAGTGTCA  
 I S Q K Q L P G V S S V

Figure 22